

SEQUENCE LISTING

<110> BASF Aktiengesellschaft

<120> Modified cytochrome P450 monooxygenases

<130> M/40434

<140>

<141>

<160> 20

<170> PatentIn Ver. 2.1

<210> 1

<211> 3150

<212> DNA

<213> Bacillus megaterium

<220>

<221> CDS

<222> (4)..(3150)

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aat tta ccg tta tta aac aca gat aaa ccg gtt caa gct ttg atg aaa	96
Asn Leu Pro Leu Leu Asn Thr Asp Lys Pro Val Gln Ala Leu Met Lys	
20 25 30	
att gcg gat gaa tta gga gaa atc ttt aaa ttc gag gcg cct ggt cgt	144
Ile Ala Asp Glu Leu Gly Glu Ile Phe Lys Phe Glu Ala Pro Gly Arg	
35 40 45	
gta acg cgc tac tta tca agt cag cgt cta att aaa gaa gca tgc gat	192
Val Thr Arg Tyr Leu Ser Ser Gln Arg Leu Ile Lys Glu Ala Cys Asp	
50 55 60	
gaa tca cgc ttt gat aaa aac tta agt caa gcg ctt aaa ttt gta cgt	240
Glu Ser Arg Phe Asp Lys Asn Leu Ser Gln Ala Leu Lys Phe Val Arg	
65 70 75	
gat ttt gca gga gac ggg tta ttt aca agc tgg acg cat gaa aaa aat	288
Asp Phe Ala Gly Asp Gly Leu Phe Thr Ser Trp Thr His Glu Lys Asn	
80 85 90 95	
tgg aaa aaa gcg cat aat atc tta ctt cca agc ttc agt cag cag gca	336
Trp Lys Lys Ala His Asn Ile Leu Leu Pro Ser Phe Ser Gln Gln Ala	
100 105 110	
atg aaa ggc tat cat gcg atg atg gtc gat atc gcc gtg cag ctt gtt	384
Met Lys Gly Tyr His Ala Met Met Val Asp Ile Ala Val Gln Leu Val	
115 120 125	
caa aag tgg gag cgt cta aat gca gat gag cat att gaa gta ccg gaa	432
Gln Lys Trp Glu Arg Leu Asn Ala Asp Glu His Ile Glu Val Pro Glu	
130 135 140	
gac atg aca cgt tta acg ctt gat aca att ggt ctt tgc ggc ttt aac	480
Asp Met Thr Arg Leu Thr Leu Asp Thr Ile Gly Leu Cys Gly Phe Asn	

145	150	155	
tat cgc ttt aac agc ttt tac cga gat cag cct cat cca ttt att aca			528
Tyr Arg Phe Asn Ser Phe Tyr Arg Asp Gln Pro His Pro Phe Ile Thr			
160	165	170	175
agt atg gtc cgt gca ctg gat gaa gca atg aac aag ctg cag cga gca			576
Ser Met Val Arg Ala Leu Asp Glu Ala Met Asn Lys Leu Gln Arg Ala			
	180	185	190
aat cca gac gac cca gct tat gat gaa aac aag cgc cag ttt caa gaa			624
Asn Pro Asp Asp Pro Ala Tyr Asp Glu Asn Lys Arg Gln Phe Gln Glu			
	195	200	205
gat atc aag gtg atg aac gac cta gta gat aaa att att gca gat cgc			672
Asp Ile Lys Val Met Asn Asp Leu Val Asp Lys Ile Ile Ala Asp Arg			
	210	215	220
aaa gca agc ggt gaa caa agc gat gat tta tta acg cat atg cta aac			720
Lys Ala Ser Gly Glu Gln Ser Asp Asp Leu Leu Thr His Met Leu Asn			
	225	230	235
gga aaa gat cca gaa acg ggt gag ccg ctt gat gac gag aac att cgc			768
Gly Lys Asp Pro Glu Thr Gly Glu Pro Leu Asp Asp Glu Asn Ile Arg			
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tat caa att att aca ttc tta att gcg gga cac gaa aca aca agt ggt			816
Tyr Gln Ile Ile Thr Phe Leu Ile Ala Gly His Glu Thr Thr Ser Gly			
	260	265	270
ctt tta tca ttt gcg ctg tat ttc tta gtg aaa aat cca cat gta tta			864
Leu Leu Ser Phe Ala Leu Tyr Phe Leu Val Lys Asn Pro His Val Leu			
	275	280	285
caa aaa gca gca gaa gaa gca gca cga gtt cta gta gat cct gtt cca			912
Gln Lys Ala Ala Glu Glu Ala Ala Arg Val Leu Val Asp Pro Val Pro			
	290	295	300
agc tac aaa caa gtc aaa cag ctt aaa tat gtc ggc atg gtc tta aac			960
Ser Tyr Lys Gln Val Lys Gln Leu Lys Tyr Val Gly Met Val Leu Asn			
	305	310	315
gaa gcg ctg cgc tta tgg cca act gct cct gcg ttt tcc cta tat gca			1008
Glu Ala Leu Arg Leu Trp Pro Thr Ala Pro Ala Phe Ser Leu Tyr Ala			
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aaa gaa gat acg gtg ctt gga gga gaa tat cct tta gaa aaa ggc gac			1056
Lys Glu Asp Thr Val Leu Gly Gly Glu Tyr Pro Leu Glu Lys Gly Asp			
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gaa cta atg gtt ctg att cct cag ctt cac cgt gat aaa aca att tgg			1104
Glu Leu Met Val Leu Ile Pro Gln Leu His Arg Asp Lys Thr Ile Trp			
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gga gac gat gtg gaa gag ttc cgt cca gag cgt ttt gaa aat cca agt			1152
Gly Asp Asp Val Glu Glu Phe Arg Pro Glu Arg Phe Glu Asn Pro Ser			
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gcg att ccg cag cat gcg ttt aaa ccg ttt gga aac ggt cag cgt gcg			1200
Ala Ile Pro Gln His Ala Phe Lys Pro Phe Gly Asn Gly Gln Arg Ala			
	385	390	395
tgt atc ggt cag cag ttc gct ctt cat gaa gca acg ctg gta ctt ggt			1248

Cys 400	Ile	Gly	Gln	Gln	Phe	Ala	Leu	His	Glu	Ala	Thr	Leu	Val	Leu	Gly	415	
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Met	Met	Leu	Lys	His	Phe	Asp	Phe	Glu	Asp	His	Thr	Asn	Tyr	Glu	Leu		
				420					425					430			
gat	att	aaa	gaa	act	tta	acg	tta	aaa	cct	gaa	ggc	ttt	gtg	gta	aaa	1344	
Asp	Ile	Lys	Glu	Thr	Leu	Thr	Leu	Lys	Pro	Glu	Gly	Phe	Val	Val	Lys		
			435					440					445				
gca	aaa	tcg	aaa	aaa	att	ccg	ctt	ggc	ggg	att	cct	tca	cct	agc	act	1392	
Ala	Lys	Ser	Lys	Lys	Ile	Pro	Leu	Gly	Gly	Ile	Pro	Ser	Pro	Ser	Thr		
		450					455				460						
gaa	cag	tct	gct	aaa	aaa	gta	cgc	aaa	aag	gca	gaa	aac	gct	cat	aat	1440	
Glu	Gln	Ser	Ala	Lys	Lys	Val	Arg	Lys	Lys	Ala	Glu	Asn	Ala	His	Asn		
	465					470					475						
acg	ccg	ctg	ctt	gtg	cta	tac	ggg	tca	aat	atg	gga	aca	gct	gaa	gga	1488	
Thr	Pro	Leu	Leu	Val	Leu	Tyr	Gly	Ser	Asn	Met	Gly	Thr	Ala	Glu	Gly		
480					485				490						495		
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Thr	Ala	Arg	Asp	Leu	Ala	Asp	Ile	Ala	Met	Ser	Lys	Gly	Phe	Ala	Pro		
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cag	gtc	gca	acg	ctt	gat	tca	cac	gcc	gga	aat	ctt	ccg	cgc	gaa	gga	1584	
Gln	Val	Ala	Thr	Leu	Asp	Ser	His	Ala	Gly	Asn	Leu	Pro	Arg	Glu	Gly		
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gct	gta	tta	att	gta	acg	gcg	tct	tat	aac	ggg	cat	ccg	cct	gat	aac	1632	
Ala	Val	Leu	Ile	Val	Thr	Ala	Ser	Tyr	Asn	Gly	His	Pro	Pro	Asp	Asn		
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Lys	Gly	Val	Arg	Tyr	Ser	Val	Phe	Gly	Cys	Gly	Asp	Lys	Asn	Trp	Ala		
560					565				570						575		
act	acg	tat	caa	aaa	gtg	cct	gct	ttt	atc	gat	gaa	acg	ctt	gcc	gct	1776	
Thr	Thr	Tyr	Gln	Lys	Val	Pro	Ala	Phe	Ile	Asp	Glu	Thr	Leu	Ala	Ala		
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Lys	Gly	Ala	Glu	Asn	Ile	Ala	Asp	Arg	Gly	Glu	Ala	Asp	Ala	Ser	Asp		
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gac	ttt	gaa	ggc	aca	tat	gaa	gaa	tgg	cgt	gaa	cat	atg	t				

Ala Lys Met His Gly Ala Phe Ser Thr Asn Val Val Ala Ser Lys Glu	660	665	670	
ctt caa cag cca ggc agt gca cga agc acg cga cat ctt gaa att gaa				2064
Leu Gln Gln Pro Gly Ser Ala Arg Ser Thr Arg His Leu Glu Ile Glu	675	680	685	
ctt cca aaa gaa gct tct tat caa gaa gga gat cat tta ggt gtt att				2112
Leu Pro Lys Glu Ala Ser Tyr Gln Glu Gly Asp His Leu Gly Val Ile	690	695	700	
cct cgc aac tat gaa gga ata gta aac cgt gta aca gca agg ttc ggc				2160
Pro Arg Asn Tyr Glu Gly Ile Val Asn Arg Val Thr Ala Arg Phe Gly	705	710	715	
cta gat gca tca cag caa atc cgt ctg gaa gca gaa gaa gaa aaa tta				2208
Leu Asp Ala Ser Gln Gln Ile Arg Leu Glu Ala Glu Glu Glu Lys Leu	720	725	730	735
gct cat ttg cca ctc gct aaa aca gta tcc gta gaa gag ctt ctg caa				2256
Ala His Leu Pro Leu Ala Lys Thr Val Ser Val Glu Glu Leu Leu Gln	740	745	750	
tac gtg gag ctt caa gat cct gtt acg cgc acg cag ctt cgc gca atg				2304
Tyr Val Glu Leu Gln Asp Pro Val Thr Arg Thr Gln Leu Arg Ala Met	755	760	765	
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Ala Ala Lys Thr Val Cys Pro Pro His Lys Val Glu Leu Glu Ala Leu	770	775	780	
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Leu Glu Lys Gln Ala Tyr Lys Glu Gln Val Leu Ala Lys Arg Leu Thr	785	790	795	
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Met Leu Glu Leu Leu Glu Lys Tyr Pro Ala Cys Glu Met Lys Phe Ser	800	805	810	815
gaa ttt atc gcc ctt ctg cca agc ata cgc ccg cgc tat tac tcg att				2496
Glu Phe Ile Ala Leu Leu Pro Ser Ile Arg Pro Arg Tyr Tyr Ser Ile	820	825	830	
tct tca tca cct cgt gtc gat gaa aaa caa gca agc atc acg gtc agc				2544
Ser Ser Ser Pro Arg Val Asp Glu Lys Gln Ala Ser Ile Thr Val Ser	835	840	845	
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Val Val Ser Gly Glu Ala Trp Ser Gly Tyr Gly Glu Tyr Lys Gly Ile	850	855	860	
gcg tcg aac tat ctt gcc gag ctg caa gaa gga gat acg att acg tgc				2640
Ala Ser Asn Tyr Leu Ala Glu Leu Gln Glu Gly Asp Thr Ile Thr Cys	865	870	875	
ttt att tcc aca ccg cag tca gaa ttt acg ctg cca aaa gac cct gaa				2688
Phe Ile Ser Thr Pro Gln Ser Glu Phe Thr Leu Pro Lys Asp Pro Glu	880	885	890	895
acg ccg ctt atc atg gtc gga ccg gga aca ggc gtc gcg ccg ttt aga				2736
Thr Pro Leu Ile Met Val Gly Pro Gly Thr Gly Val Ala Pro Phe Arg	900	905	910	
ggc ttt gtg cag gcg cgc aaa cag cta aaa gaa caa gga cag tca ctt				2784

Gly Phe Val Gln Ala Arg Lys Gln Leu Lys Glu Gln Gly Gln Ser Leu	
915 920 925	
gga gaa gca cat tta tac ttc ggc tgc cgt tca cct cat gaa gac tat	2832
Gly Glu Ala His Leu Tyr Phe Gly Cys Arg Ser Pro His Glu Asp Tyr	
930 935 940	
ctg tat caa gaa gag ctt gaa aac gcc caa agc gaa ggc atc att acg	2880
Leu Tyr Gln Glu Glu Leu Glu Asn Ala Gln Ser Glu Gly Ile Ile Thr	
945 950 955	
ctt cat acc gct ttt tct cgc atg cca aat cag ccg aaa aca tac gtt	2928
Leu His Thr Ala Phe Ser Arg Met Pro Asn Gln Pro Lys Thr Tyr Val	
960 965 970 975	
cag cac gta atg gaa caa gac ggc aag aaa ttg att gaa ctt ctt gat	2976
Gln His Val Met Glu Gln Asp Gly Lys Lys Leu Ile Glu Leu Leu Asp	
980 985 990	
caa gga gcg cac ttc tat att tgc gga gac gga agc caa atg gca cct	3024
Gln Gly Ala His Phe Tyr Ile Cys Gly Asp Gly Ser Gln Met Ala Pro	
995 1000 1005	
gcc gtt gaa gca acg ctt atg aaa agc tat gct gac gtt cac caa gtg	3072
Ala Val Glu Ala Thr Leu Met Lys Ser Tyr Ala Asp Val His Gln Val	
1010 1015 1020	
agt gaa gca gac gct cgc tta tgg ctg cag cag cta gaa gaa aaa ggc	3120
Ser Glu Ala Asp Ala Arg Leu Trp Leu Gln Gln Leu Glu Glu Lys Gly	
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<211> 1048

<212> PRT

<213> Bacillus megaterium

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Ala Asp Glu Leu Gly Glu Ile Phe Lys Phe Glu Ala Pro Gly Arg Val	
35 40 45	
Thr Arg Tyr Leu Ser Ser Gln Arg Leu Ile Lys Glu Ala Cys Asp Glu	
50 55 60	
Ser Arg Phe Asp Lys Asn Leu Ser Gln Ala Leu Lys Phe Val Arg Asp	
65 70 75 80	
Phe Ala Gly Asp Gly Leu Phe Thr Ser Trp Thr His Glu Lys Asn Trp	
85 90 95	
Lys Lys Ala His Asn Ile Leu Leu Pro Ser Phe Ser Gln Gln Ala Met	
100 105 110	
Lys Gly Tyr His Ala Met Met Val Asp Ile Ala Val Gln Leu Val Gln	

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Arg	Phe	Asn	Ser	Phe	Tyr	Arg	Asp	Gln	Pro	His	Pro	Phe	Ile	Thr	Ser
				165					170					175	
Met	Val	Arg	Ala	Leu	Asp	Glu	Ala	Met	Asn	Lys	Leu	Gln	Arg	Ala	Asn
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Pro	Asp	Asp	Pro	Ala	Tyr	Asp	Glu	Asn	Lys	Arg	Gln	Phe	Gln	Glu	Asp
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Ile	Lys	Val	Met	Asn	Asp	Leu	Val	Asp	Lys	Ile	Ile	Ala	Asp	Arg	Lys
210						215					220				
Ala	Ser	Gly	Glu	Gln	Ser	Asp	Asp	Leu	Leu	Thr	His	Met	Leu	Asn	Gly
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Lys	Asp	Pro	Glu	Thr	Gly	Glu	Pro	Leu	Asp	Asp	Glu	Asn	Ile	Arg	Tyr
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Gln	Ile	Ile	Thr	Phe	Leu	Ile	Ala	Gly	His	Glu	Thr	Thr	Ser	Gly	Leu
			260					265						270	
Leu	Ser	Phe	Ala	Leu	Tyr	Phe	Leu	Val	Lys	Asn	Pro	His	Val	Leu	Gln
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Lys	Ala	Ala	Glu	Glu	Ala	Ala	Arg	Val	Leu	Val	Asp	Pro	Val	Pro	Ser
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Tyr	Lys	Gln	Val	Lys	Gln	Leu	Lys	Tyr	Val	Gly	Met	Val	Leu	Asn	Glu
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Ala	Leu	Arg	Leu	Trp	Pro	Thr	Ala	Pro	Ala	Phe	Ser	Leu	Tyr	Ala	Lys
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Glu	Asp	Thr	Val	Leu	Gly	Gly	Glu	Tyr	Pro	Leu	Glu	Lys	Gly	Asp	Glu
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Leu	Met	Val	Leu	Ile	Pro	Gln	Leu	His	Arg	Asp	Lys	Thr	Ile	Trp	Gly
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Asp	Asp	Val	Glu	Glu	Phe	Arg	Pro	Glu	Arg	Phe	Glu	Asn	Pro	Ser	Ala
		370				375					380				
Ile	Pro	Gln	His	Ala	Phe	Lys	Pro	Phe	Gly	Asn	Gly	Gln	Arg	Ala	Cys
385						390					395				400
Ile	Gly	Gln	Gln	Phe	Ala	Leu	His	Glu	Ala	Thr	Leu	Val	Leu	Gly	Met
				405					410					415	
Met	Leu	Lys	His	Phe	Asp	Phe	Glu	Asp	His	Thr	Asn	Tyr	Glu	Leu	Asp
			420					425					430		
Ile	Lys	Glu	Thr	Leu	Thr	Leu	Lys	Pro	Glu	Gly	Phe	Val	Val	Lys	Ala
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Lys	Ser	Lys	Lys	Ile	Pro	Leu	Gly	Gly	Ile	Pro	Ser	Pro	Ser	Thr	Glu
						455					460				

Gln Ser Ala Lys Lys Val Arg Lys Lys Ala Glu Asn Ala His Asn Thr
 465 470 475 480
 Pro Leu Leu Val Leu Tyr Gly Ser Asn Met Gly Thr Ala Glu Gly Thr
 485 490 495
 Ala Arg Asp Leu Ala Asp Ile Ala Met Ser Lys Gly Phe Ala Pro Gln
 500 505 510
 Val Ala Thr Leu Asp Ser His Ala Gly Asn Leu Pro Arg Glu Gly Ala
 515 520 525
 Val Leu Ile Val Thr Ala Ser Tyr Asn Gly His Pro Pro Asp Asn Ala
 530 535 540
 Lys Gln Phe Val Asp Trp Leu Asp Gln Ala Ser Ala Asp Glu Val Lys
 545 550 555 560
 Gly Val Arg Tyr Ser Val Phe Gly Cys Gly Asp Lys Asn Trp Ala Thr
 565 570 575
 Thr Tyr Gln Lys Val Pro Ala Phe Ile Asp Glu Thr Leu Ala Ala Lys
 580 585 590
 Gly Ala Glu Asn Ile Ala Asp Arg Gly Glu Ala Asp Ala Ser Asp Asp
 595 600 605
 Phe Glu Gly Thr Tyr Glu Glu Trp Arg Glu His Met Trp Ser Asp Val
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 Ala Ala Tyr Phe Asn Leu Asp Ile Glu Asn Ser Glu Asp Asn Lys Ser
 625 630 635 640
 Thr Leu Ser Leu Gln Phe Val Asp Ser Ala Ala Asp Met Pro Leu Ala
 645 650 655
 Lys Met His Gly Ala Phe Ser Thr Asn Val Val Ala Ser Lys Glu Leu
 660 665 670
 Gln Gln Pro Gly Ser Ala Arg Ser Thr Arg His Leu Glu Ile Glu Leu
 675 680 685
 Pro Lys Glu Ala Ser Tyr Gln Glu Gly Asp His Leu Gly Val Ile Pro
 690 695 700
 Arg Asn Tyr Glu Gly Ile Val Asn Arg Val Thr Ala Arg Phe Gly Leu
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 Asp Ala Ser Gln Gln Ile Arg Leu Glu Ala Glu Glu Glu Lys Leu Ala
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 His Leu Pro Leu Ala Lys Thr Val Ser Val Glu Glu Leu Leu Gln Tyr
 740 745 750
 Val Glu Leu Gln Asp Pro Val Thr Arg Thr Gln Leu Arg Ala Met Ala
 755 760 765
 Ala Lys Thr Val Cys Pro Pro His Lys Val Glu Leu Glu Ala Leu Leu
 770 775 780
 Glu Lys Gln Ala Tyr Lys Glu Gln Val Leu Ala Lys Arg Leu Thr Met
 785 790 795 800
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805	810	815
Phe Ile Ala Leu Leu Pro Ser Ile	Arg Pro Arg Tyr Tyr Ser Ile Ser	
820	825	830
Ser Ser Pro Arg Val Asp Glu Lys Gln Ala Ser Ile Thr Val Ser Val		
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Val Ser Gly Glu Ala Trp Ser Gly Tyr Gly Glu Tyr Lys Gly Ile Ala		
850	855	860
Ser Asn Tyr Leu Ala Glu Leu Gln Glu Gly Asp Thr Ile Thr Cys Phe		
865	870	875
Ile Ser Thr Pro Gln Ser Glu Phe Thr Leu Pro Lys Asp Pro Glu Thr		
885	890	895
Pro Leu Ile Met Val Gly Pro Gly Thr Gly Val Ala Pro Phe Arg Gly		
900	905	910
Phe Val Gln Ala Arg Lys Gln Leu Lys Glu Gln Gly Gln Ser Leu Gly		
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Glu Ala His Leu Tyr Phe Gly Cys Arg Ser Pro His Glu Asp Tyr Leu		
930	935	940
Tyr Gln Glu Glu Leu Glu Asn Ala Gln Ser Glu Gly Ile Ile Thr Leu		
945	950	955
His Thr Ala Phe Ser Arg Met Pro Asn Gln Pro Lys Thr Tyr Val Gln		
965	970	975
His Val Met Glu Gln Asp Gly Lys Lys Leu Ile Glu Leu Leu Asp Gln		
980	985	990
Gly Ala His Phe Tyr Ile Cys Gly Asp Gly Ser Gln Met Ala Pro Ala		
995	1000	1005
Val Glu Ala Thr Leu Met Lys Ser Tyr Ala Asp Val His Gln Val Ser		
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<210> 3

<211> 30

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: PCR primer

<400> 3

gcaggagacg gggtgnnnac aagctggacg

30

<210> 4

<211> 30

<212> DNA

<213> Artificial sequence

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<223> Description of the artificial sequence: PCR primer

<400> 4

cgtccagctt gtanncaacc cgtctcctgc

30

<210> 5

<211> 34

<212> DNA

<213> Artificial sequence

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<223> Description of the artificial sequence: PCR primer

<400> 5

gaagcaatga acaagannca gcgagcaaat ccag

34

<210> 6

<211> 34

<212> DNA

<213> Artificial sequence

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<223> Description of the artificial sequence: PCR primer

<400> 6

ctggatttgc tcgtgannnc ttgttcattg cttc

34

<210> 7

<211> 41

<212> DNA

<213> Artificial sequence

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<223> Description of the artificial sequence: PCR primer

<400> 7

gctttgataa aaacttaaag tcaannnctt aaatttgtac g

41

<210> 8

<211> 40

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: PCR primer

<400> 8

cgtacaaatt taagnnnttg acttaagttt ttatcaaagc

40

<210> 9

<211> 37

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: PCR primer

<400> 9

gttatttaa acagataaan nngttcaagc ttgatg

37

<210> 10

<211> 37

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: PCR primer

<400> 10

catcaaagct tgaacnnntt tatctgtggt taataac

37

<210> 11

<211> 37

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: PCR primer

<400> 11

gttatttaa acagataaac cgnnncaagc ttgatg

37

<210> 12

<211> 37

<212> DNA

<213> Artificial sequence

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<223> Description of the artificial sequence: PCR primer

<400> 12

catcaaagct tgnnncggtt tatctgtggt taataac

37

<210> 13

<211> 33

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: PCR primer

<400> 13

cgaggcgctt ggtnnnngtaa cgcgtactt atc

33

<210> 14

<211> 33

<212> DNA

<213> Artificial sequence

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<223> Description of the artificial sequence: PCR-primer

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gataagtagc gcgttacnnn accaggcgcc tcg

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<210> 15

<211> 34
<212> DNA
<213> Artificial sequence

<220>

<223> Description of the artificial sequence: PCR primer

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<210> 16
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<212> DNA
<213> Artificial sequence

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<223> Description of the artificial sequence: PCR primer

<400> 16
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<210> 17
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<213> Artificial sequence

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<223> Description of the artificial sequence: PCR primer

<400> 17
gctttgataa aaacttannn caagcgctta aatttgtacg

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<210> 18
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<213> Artificial sequence

<220>

<223> Description of the artificial sequence: PCR primer

<400> 18
cgtacaaatt taagcgcttg nnntaagttt ttatcaaagc

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<210> 19
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<212> DNA
<213> Artificial sequence

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<223> Description of the artificial sequence: PCR primer

<400> 19
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<223> Description of the artificial sequence: PCR primer

<400> 20

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SEQUENCE LISTING

<110> Hauer, Bernhard
 Pleiss, Jurgen
 Schwaneberg, Ulrich
 Schmitt, Jutta

<120> Modified cytochrome P450 monooxygenases

<130> M/40434

<140> US 10/031,695

<150> PCT/EP00/07252

<151> 2000-07-27

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Asn	Leu	Pro	Leu	Leu	Asn	Thr	Asp	Lys	Pro	Val	Gln	Ala	Leu	Met	Lys	
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Ile	Ala	Asp	Glu	Leu	Gly	Glu	Ile	Phe	Lys	Phe	Glu	Ala	Pro	Gly	Arg	
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Asp	Phe	Ala	Gly	Asp	Gly	Leu	Phe	Thr	Ser	Trp	Thr	His	Glu	Lys	Asn	
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Trp	Lys	Lys	Ala	His	Asn	Ile	Leu	Leu	Pro	Ser	Phe	Ser	Gln	Gln	Ala	
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Ser Met Val Arg Ala Leu Asp Glu Ala Met Asn Lys Leu Gln Arg Ala	
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Gln Lys Ala Ala Glu Glu Ala Ala Arg Val Leu Val Asp Pro Val Pro	
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Asp Ile Lys Glu Thr Leu Thr Leu Lys Pro Glu Gly Phe Val Val Lys	
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Gln Val Ala Thr Leu Asp Ser His Ala Gly Asn Leu Pro Arg Glu Gly	
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Ala Lys Met His Gly Ala Phe Ser Thr Asn Val Val Ala Ser Lys Glu	
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Pro Arg Asn Tyr Glu Gly Ile Val Asn Arg Val Thr Ala Arg Phe Gly	
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770 775 780	
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Val Val Ser Gly Glu Ala Trp Ser Gly Tyr Gly Glu Tyr Lys Gly Ile	
850 855 860	
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<212> PRT

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Lys Lys Ala His Asn Ile Leu Leu Pro Ser Phe Ser Gln Gln Ala Met
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Lys Gly Tyr His Ala Met Met Val Asp Ile Ala Val Gln Leu Val Gln
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Pro Asp Asp Pro Ala Tyr Asp Glu Asn Lys Arg Gln Phe Gln Glu Asp
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Ile Lys Val Met Asn Asp Leu Val Asp Lys Ile Ile Ala Asp Arg Lys
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 <221> unsure
 <222> 1..30
 <223> n is a or g or c or t/u, unknown, or other

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 <223> n is a or g or c or t/u, unknown, or other

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 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence: PCR primer

<221> unsure
 <222> 1..33
 <223> n is a or g or c or t/u, unknown, or other

<400> 13
 cgaggcgctt ggtnnngtaa cgcgctactt atc

33

<210> 14
 <211> 33
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence: PCR-primer

<221> unsure
 <222> 1..33
 <223> n is a or g or c or t/u, unknown, or other

<400> 14

gataagtagc gcgttacnnn accaggcgcc tcg

33

<210> 15
 <211> 34
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence: PCR primer

<221> unsure
 <222> 1..34
 <223> n is a or g or c or t/u, unknown, or other

<400> 15

cctggctcgtg taacgcgcnn nttatcaagt cagc

34

<210> 16

<211> 34

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: PCR primer

<221> unsure

<222> 1..34

<223> n is a or g or c or t/u, unknown, or other

<400> 16

gctgacttga taannngcgc gttacacgac cagg

34

<210> 17

<211> 40

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: PCR primer

<221> unsure

<222> 1..40

<223> n is a or g or c or t/u, unknown, or other

<400> 17

gctttgataa aaacttannn caagcgctta aatttgtagc

40

<210> 18

<211> 40

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: PCR primer

<221> unsure

<222> 1..40

<223> n is a or g or c or t/u, unknown, or other

<400> 18

cgtacaaatt taagcgcttg nnntaagttt ttatcaaagc

40

<210> 19

<211> 30

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: PCR primer

<221> unsure
<222> 1..30
<223> n is a or g or c or t/u, unknown, or other

<400> 19

ggcgacgaac tannngttct gattcctcag

30

<210> 20
<211> 30
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: PCR primer

<221> unsure
<222> 1..30
<223> n is a or g or c or t/u, unknown, or other

<400> 20

ctgaggaatc agaacnnnta gttcgtcgcc

30